

Human G70 cDNA (SEQ ID NO 1)

Length:	1465 bp				
1_	_GCCAACCTTG	-CCTCCCCAA	-CCCTGGGGCC	GCCCCAGGGT	TCCTGCGCAC
51	TGCCTGTTCC	TCCTGGGTGT	CACTGGCAGC	CCTGTCCTTC	CTAGAGGGAC
101	TGGAACCTAA		GCTGAGGGAG		CTCAAGGCAA
151	CGCTGGCCCC	ACGÁCGGAGT	GCCAGGAGCA	CTAACAGTAC	CCTTAGCTTG
201	CTTTCCTCCT	CCCTCCTTTT	TATTTTCAAG	TTCCTTTTTA	TTTCTCCTTG
251	CGTAACAACC	TTCTTCCCTT	CTGCACCACT	GCCCGTACCC	TTACCCGCCC
301	CGCCACCTCC	TTGCTACCCC	ACTCTTGAAA	CCACAGCTGT	TGGCAGGGTC
351	CCCAGCTCAT	GCCAGCCTCA	TCTCCTTTCT	TGCTAGCCCC	CAAAGGGCCT
401	CCAGGCAACA	TGGGGGGCCC	AGTCAGAGAG	CCGGCACTCT	CAGTTGCCCT
451	CTGGTTGAGT	TGGGGGGCAG	CTCTGGGGGC	CGTGGCTTGT	GCCATGGCTC
501	TGCTGACCCA	ACAAACAGAG	CTGCAGAGCC	TCAGGAGAGA	GGTGAGCCGG
551	CTGCAGGGGA	CAGGAGGCCC	CTCCCAGAAT	GGGGAAGGGT	ATCCCTGGCA
601	GAGTCTCCCG	GAGCAGAGTT	CCGATGCCCT	GGAAGCCTGG	GAGAGTGGGG
651	AGAGATCCCG	GAAAAGGAGA	GCAGTGCTCA	CCCAAAAACA	GAAGAAGCAG
701	CACTCTGTCC	TGCACCTGGT	TCCCATTAAC	GCCACCTCCA	AGGATGACTC
751	CGATGTGACA	GAGGTGATGT	GGCAACCAGC	TCTTAGGCGT	GGGAGAGGCC
801	TACAGGCCCA	AGGATATGGT	GTCCGAATCC	AGGATGCTGG	AGTTTATCTG
851	CTGTATAGCC	AGGTCCTGTT	TCAAGACGTG	ACTTTCACCA	TGGGTCAGGT
901	GGTGTCTCGA	GAAGGCCAAG	GAAGGCAGGA	GACTCTATTC	CGATGTATAA
951	GAAGTATGCC	CTCCCACCCG	GACCGGGCCT	ACAACAGCTG	CTATAGCGCA
1001	GGTGTCTTCC	ATTTACACCA	AGGGGATATT	CTGAGTGTCA	TAATTCCCCG
1051	GGCAAGGGCG	AAACTTAACC	TCTCTCCACA	TGGAACCTTC	CTGGGGTTTG
1101	TGAAACTGTG	ATTGTGTTAT	AAAAAGTGGC	TCCCAGCTTG	GAAGACCAGG
1151	GTGGGTACAT	ACTGGAGACA	GCCAAGAGCT	GAGTATATAA	AGGAGAGGGA
1201	ATGTGCAGGA	ACAGAGGCGT	CTTCCTGGGT	TTGGCTCCCC	GTTCCTCACT
1251	TTTCCCTTTT	CATTCCCACC	CCCTAGACTT	TGATTTTACG	GATATCTTGC
1301	TTCTGTTCCC	CATGGAGCTC	CGAATTCTTG	CGTGTGTGTA	GATGAGGGGC
1351	GGGGGACGGG	CGCCAGGCAT	TGTTCAGACC	TGGTCGGGGC	CCACTGGAAG
1401	CATCCAGAAC	AGCACCACCA	TCTAACGGCC	GCTCGAGGGA	AGCACCCGGC
1451	GGTTTGGGCG	AAGTC			

The proposed transmembrane domains are boxed

human G70 protein sequence (SEQ ID NO 2)

- 1 MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT
- 51 QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS
- 101 RKRRAVLTQK QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA
- 151 QGYGVRIQDA GVYLLYSQVL FQDVTFTMGQ VVSREGQGRQ ETLFRCIRSM
- 201 PSHPDRAYNS CYSAGVFHLH QGDILSVIIP RARAKLNLSP HGTFLGFVKL

Figure 2A Sequence of mouse G70 (SEQ ID NOS: 3 and 4)

Mouse G70 (SEQ ID NO 3)
1 CATGCCGAGT GCTTTGTGTG TGTTACCTGC TCTAAGAAGC TGGCTGGGCA

-	ciiiocconoi G	CITIGIGIG I	GITACCIGC I	CIAAGAAGC 1	GGCTGGGCA
51	GCGTTTCACC	GCTGTGGAGG	-ACCAGTATTA	CTGCGTGGAT	TGCTACAAGA
101	ACTTTGTGGC	CAAGAAGTGT	GCTGGATGCA	AGAACCCCAT	CACTGGGTTT
151	GGTAAAGGCT	CCAGTGTGGT	GGCCTATGAA	GGACAATCCT	GGCACGACTA
201	CTGCTTCCAC	TGCAAAAAAT	GCTCCGTGAA	TCTGGCCAAC	AAGCGCTTTG
251	TATTTCATAA	TGAGCAGGTG	TATTGCCCTG	ACTGTGCCAA	AAAGCTGTAA
301	CTTGACGGCT	GCCCTGTCCT	TCCTAGATAA	TGGCACCAAA	TTCTCCTGAG
351	GCTAGGGGGG	AAGGAGTGTC	AGAGTGTCAC	TAGCTCGACC	CTGGGGACAA
401	GGGGGACTAA	TAGTACCCTA	GCTTGATTTC	TTCCTATTCT	CAAGTTCCTT
451	TTTATTTCTC	CCTTGCGTAA	CCCGCTCTTC	CCTTCTGTGC	CTTTGCCTGT
501	ATTCCCACCC	TCCCTGCTAC	CTCTTGGCCA	CCTCACTTCT	GAGACCACAG
551	CTGTTGGCAG	GGTCCCTAGC	TC <u>ATG</u> CCAGC	CTCATCTCCA	GGCCACATGG
601	GGGGCTCAGT	CAGAGAGCCA	GCCCTTTCGG	TTGCTCTTTG	GTTGAGTTGG
651	GGGGCAGTTC	TGGGGGCTGT	GACTTGTGCT	GTCGCACTAC	TGATCCAACA
701	GACAGAGCTG	CAAAGCCTAA	GGCGGGAGGT	GAGCCGGCTG	CAGCGGAGTG
751	GAGGGCCTTC	CCAGAAGCAG	GGAGAGCGCC	CATGGCAGAG	CCTCTGGGAG
801	CAGAGTCCTG	ATGTCCTGGA	AGCCTGGAAG	GATGGGGCGA	AATCTCGGAG
851	AAGGAGAGCA	GTACTCACCC	AGAAGCACAA	GAAGAAGCAC	TCAGTCCTGC
901	ATCTTGTTCC	AGTTAACATT	ACCTCCAAGG	ACTCTGACGT	GACAGAGGTG
951	ATGTGGCAAC	CAGTACTTAG	GCGTGGGAGA	GGCCTGGAGG	CCCAGGGAGA
1001	CATTGTACGA	GTCTGGGACA	CTGGAATTTA	TCTGCTCTAT	AGTCAGGTCC
1051	TGTTTCATGA	TGTGACTTTC	ACAATGGGTC	AGGTGGTATC	TCGGGAAGGA
1101	CAAGGGAGAA	GAGAAACTCT	ATTCCGATGT	ATCAGAAGTA	TGCCTTCTGA
1151	TCCTGACCGT	GCCTACAATA	GCTGCTACAG	TGCAGGTGTC	TTTCATTTAC
1201	ATCAAGGGGA	TATTATCACT	GTCAAAATTC	CACGGGCAAA	CGCAAAACTT
1251	AGCCTTTCTC	CGCATGGAAC	ATTCCTGGGG	TTTGTGAAAC	TA <u>TGA</u> TTGTT
1301	ATAAAGGGGG	TGGGGATTTC	CCATTCCAAA	AACTGGCTAG	ACAAAGGACA
1351	AGGAACGGTC	AAGAACAGCT	CTCCATGGCT	TTGCCTTGAC	TGTTGTTCCT
1401	CCCTTTGCCT	TTCCCGCTCC	CACTATCTGG	GCTTTGACTC	CATGGATATT
1451	AAAAAAGTAG	AATATTTTGT	GTTTATCTCC	CAAAAA	•

Figure 2B

Mouse G70 Length: 241 (SEQ ID NO 4)

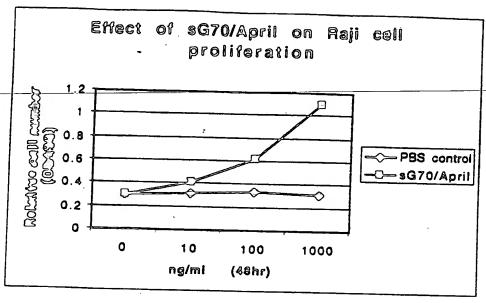
- 1 MPASSPGHMG GSVREPALSV ALWLSWGAVL GAVTCAVALL IQOTELOSLR
- 51 REVSRLQRSG GPSQKQGERP WQSLWEQSPD VLEAWKDGAK SRRRRAVLTQ
- 101 KHKKKHSVLH LVPVNITSKD SDVTEVMWQP VLRRGRGLEA QGDIVRVWDT
- 151 GIYLLYSQVL FHDVTFTMGQ VVSREGQGRR ETLFRCIRSM PSDPDRAYNS
- 201 CYSAGVFHLH QGDIITVKIP RANAKLSLSP HGTFLGFVKL *

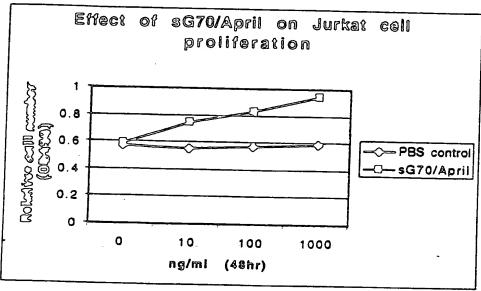
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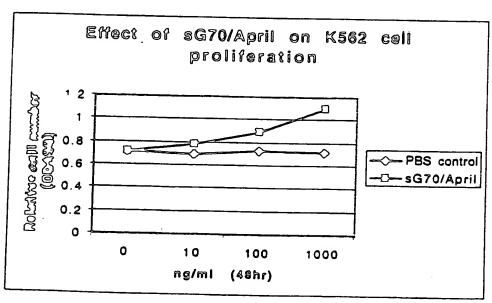
MDYKDDDDKKHKKKHSVLHLVPVNITSKDSDVTEVMWQPVLRRGRGLEAQGDIVRVW DTGIYLLYSQVLFHDVTFTMGQVVSREGQGRRETLFRCIRSMPSDPDRAYNSCYSAG VFHLHQGDIITVKIPRANAKLSLSPHGTFLGFVKL*

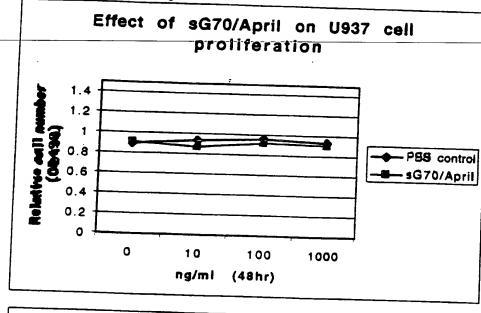
Figure 3 Alignm. of human and mouse G70

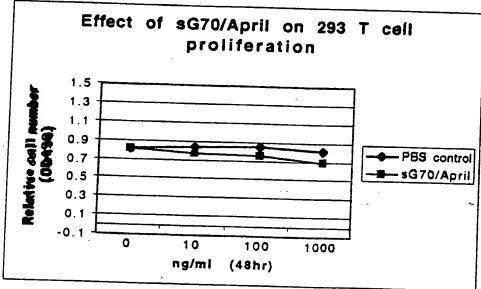
		•	
mouse:	1	MPASSPGHMGGSVREPALSVALWLSWGAVLGAVTCAVALLIQQTELQSLRR	
Human:	1	_MPASSPG+MGG_VREPALSVALWLSWGA_LGAV-CA+ALL QQTELQSLRR MPASSPFLLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRR	
mouse:	52	EVSRLQRSGGPSQKQGERPWQSLWEQSPDVLEAWKDGAKSRRRRAVLTQKHKKKHSVLHL EVSRLQ +GGPSQ PWQSL EQS D LEAW+ G +SR+RRAVLTQK KK+HSVLHL	111
human:	61	EVSRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWESGERSRKRRAVLTQKQKKQHSVLHL	120
mouse:	112	VPVNITSKD-SDVTEVMWQPVLRRGRGLEAQGDIVRVWDTGIYLLYSQVLFHDVTFTMGQ VP+N TSKD SDVTEVMWQP LRRGRGL+AQG VR+ D G+YLLYSQVLF DVTFTMGO	170
human:	121	VPINATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ	180
mouse:	171	VVSREGQGRRETLFRCIRSMPSDPDRAYNSCYSAGVFHLHQGDIITVKIPRANAKLSLSP VVSREGQGR+ETLFRCIRSMPS PDRAYNSCYSAGVFHLHQGDI++V IPRA AKL+LSP	230
human:	181	VVSREGQGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP	240
		HGTFLGFVKL 240 HGTFLGFVKL	•
human:	241	HGTFLGFVKL 250	
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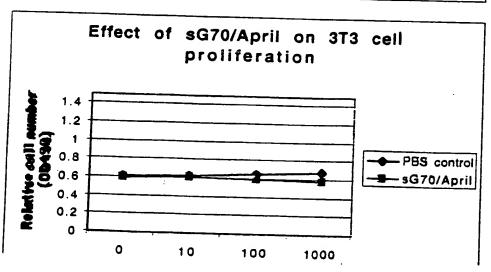


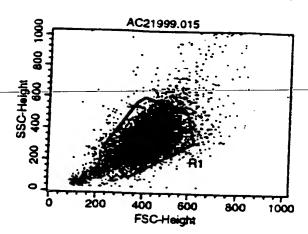




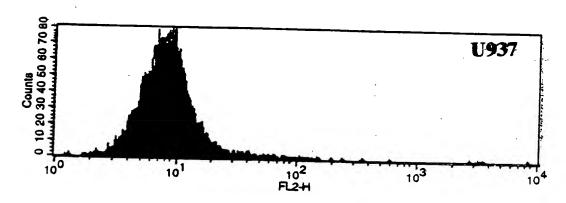


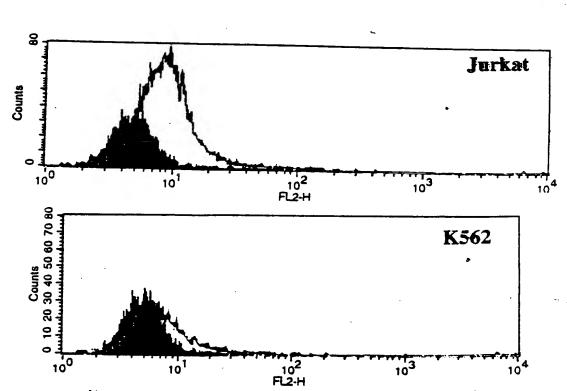
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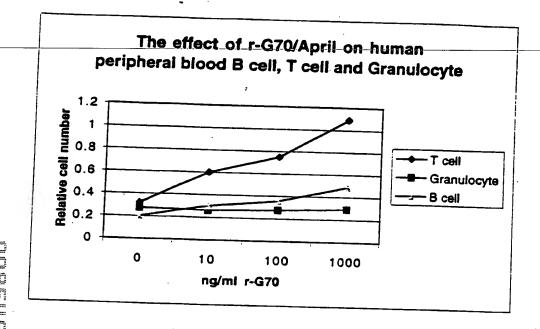




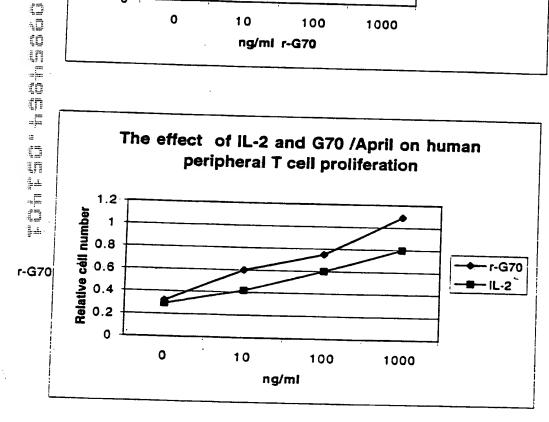
FACS analysis of G70/April receptor binding











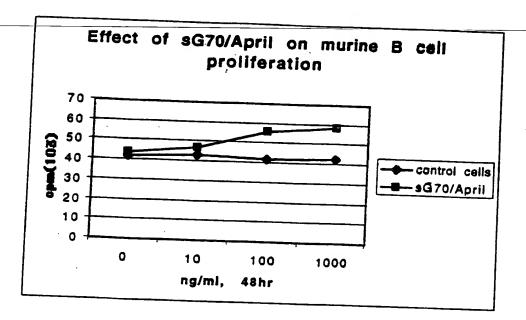


Fig. 7

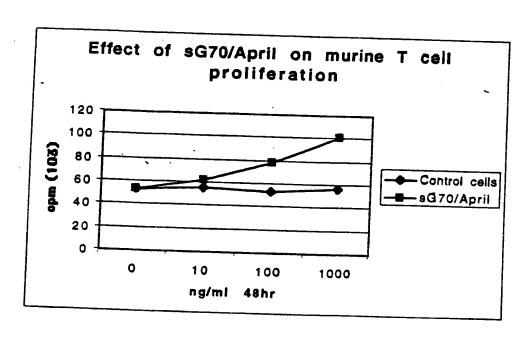


Fig. 8

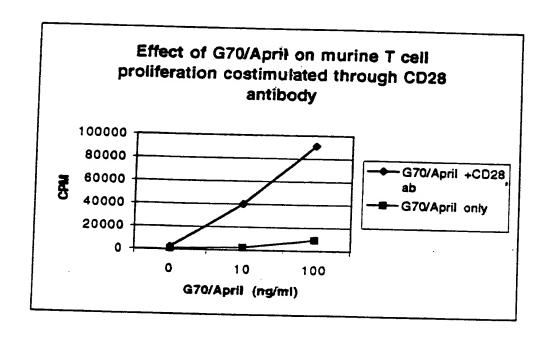


Fig. 9

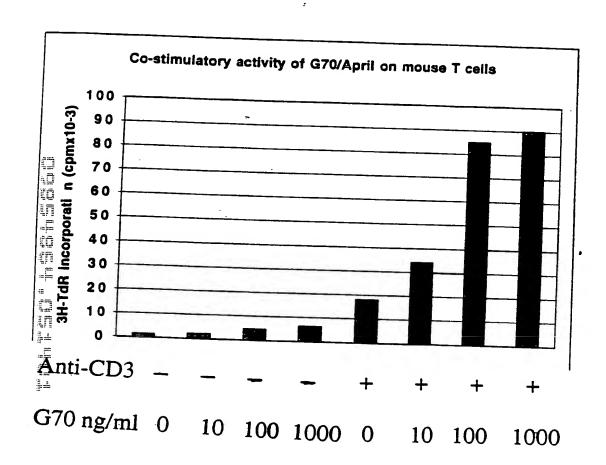


Figure 10A

Human BCMA

Human (SEQ ID NO: 5):

1 MAGQCSQNEY FDSLLHACIP CQLRCSSNTP PLTCQRYCNA SVTNSVKGTN

51 AILWTCLGLS LIISLAVFVL MFLLRKISSE PLKDEFKNTG SGLLGMANID

101 LEKSRTGDEI ILPRGLEYTV EECTCEDCIK SKPKVDSDHC FPLPAMEEGA

151 TILVTTKTND YCKSLPAALS ATEIEKSISA R

Human (SEQ ID NO: 5):

MAGQCSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY CNASVTNSVK
GTNA ILWTCL GLSLIISLAV FVLMFLLRKI SSEPLKDEFK NTGSGLLGMA
NIDLEKSRTG DEIILPRGLE YTVEECTCED CIKSKPKVDS DHCFPLPAME
EGATILVTTK TNDYCKSLPA ALSATEIEKS ISAR

hBCMA's extracellular domain (SEQ ID NO: 6):

MAGQCSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY CNASVTNSVK GTNA

hBCMA's cysteine-rich consensus region (SEQ ID NO: 7):

CSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY C

hBCMA's transmembrane region (SEQ ID NO: 8):

ILWTCL GLSLIISLAV FVLMF

Figure 10B

huBCMA-Fc (SEQ ID NO: 9):

MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA GGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK*

muBCMA-Fc (SEQ ID NO: 10):

MAQQCFHSEYFDSLLHACKPCHLRCSNPPATCQPYCDPSVTSSVKGSYTG GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK*

Sbjct:

179 EKPTHTR 185

Figure 11 Alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence

murine BCMA amino acid sequence Length: 185 (SEQ ID NO: 11):

- 1 MAQQCFHSEY FDSLLHACKP CHLRCSNPPA TCQPYCDPSV TSSVKGTYTV
- 51 LWIFLGLTLV LSLALFTISF LLRKMNPEAL KDEPQSPGQL DGSAQLDKAD
- 101 TELTRIRAGD DRIFPRSLEY TVEECTCEDC VKSKPKGDSD HFFPLPAMEE
- 151 GATILVTTKT GDYGKSSVPT ALQSVMGMEK PTHTR

alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence.

Query:	4	MAGQCSQNEYFOSILEACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS MA QC +EYFOSILEAC PC LRCS+ PP TCQ YC+ SVT+SVKGT +LW LGL+	63
Sbjct:	1	MAQQCFESEYFDSLLEACKPCHLRCSNPPATCQPYCDPSVTSSVKGTYTVLWIFLGLT	58
Query:	64	LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGL L++SLA+F + FLLRK++ E LKDE ++ G S L A+ +L + R GD+ I PR L	119
Sbjct:	59	LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL	118
Query:	120	EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKS-LPAAL-SATEI EYTVEECTCEDC+KSKPK DSDH FPLPAMEEGATILVTTKT DY KS +P AL S +	177
Sbjct:	119	EYTVEECTCEDC+KSKPK DSDH FPLPAMEEGATILVTTKT DY KS +P AL S + EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM	178
Query:	178	EKSISAR 184	

Figure 12A Human TACI

huTACI (SEQ ID NO: 14).

- 1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
 - 51 KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC
 - 101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
 - 151 PGLKLSADQV ALVYSTLGLC LCAVLCCFLV AVACFLKKRG DPCSCQPRSR
 - 201 PRQSPAKSSQ DHAMEAGSPV STSPEPVETC SFCFPECRAP TQESAVTPGT
 - 251 PDPTCAGRWG CHTRTTVLQP CPHIPDSGLG IVCVPAQEGG PGA

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSC KTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQC AYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPAL PGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSR PRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAPTQESAVTPGT PDPTCAGRWGCHTRTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

huTACI's extracellular domain (SEQ ID NO: 15):

- 1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
 - 51 KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC
 - 101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
 - 151 PGLKLSADQV ALVYST



huTACI's cysteine-rich consensus region (SEQ ID NO: 16):
CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC and
CRKEQGKFYDHLLRDCISCASICGQHPKQCAYFC

transmembrane region (SEQ ID NO: 17): LGLCLCAVLCCFLVAVACFL

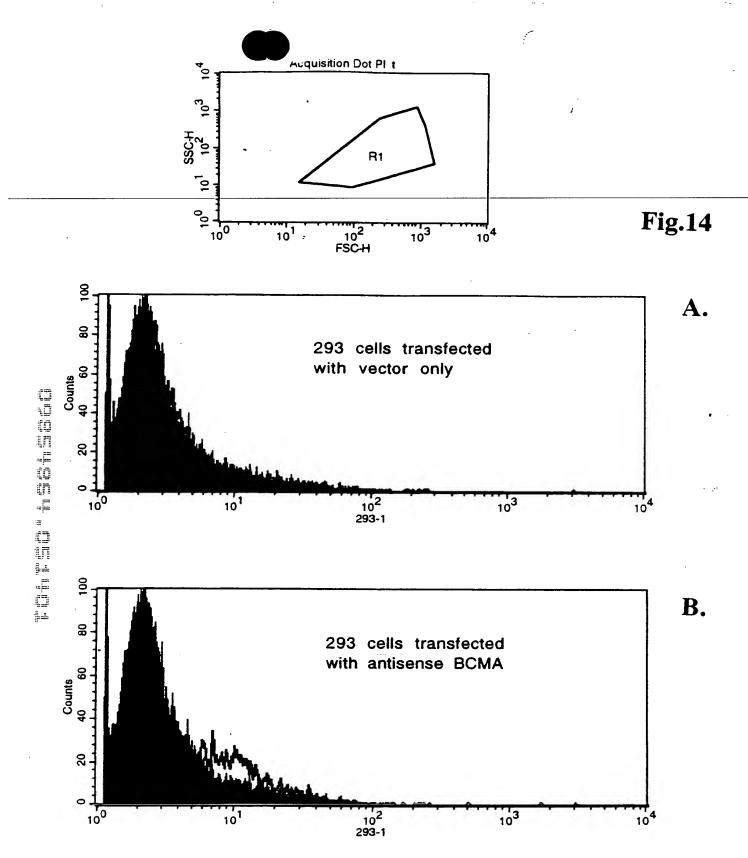
hTACI-Fc (SEQ ID NO: 18):

- 1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
 - 51 KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC
 - 101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
 - 151 PGLKLSADQV ALVYSGGGGG DKTHTCPPCP APELLGGPSV FLFPPKPKDT
 - 201 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
 - 251 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
 - 301 LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
 - 351 DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK*

Figure 13 Alignment of cysteine rich extracellular regions of human

TACI and human BCMA.

- 34 CPEEQYWDPLLGTCMSCKTICNHQS.QRTCAAFCRSLSCRKEQGKFYDHL 82 | : : | . | | | . | . | . . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . | . : . |
 - 83 LRDCISCASI 92 | |: . | 56 LWTCLGLSLI 65



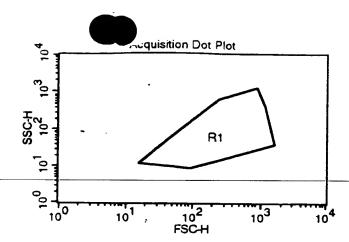
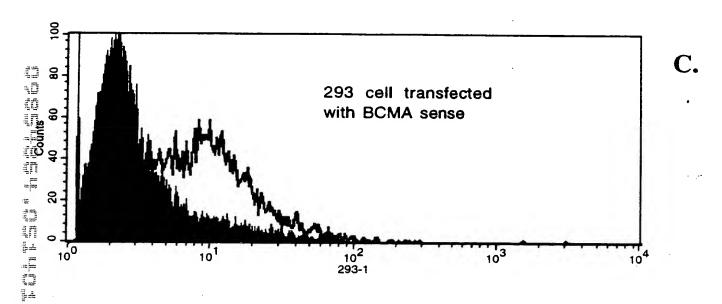


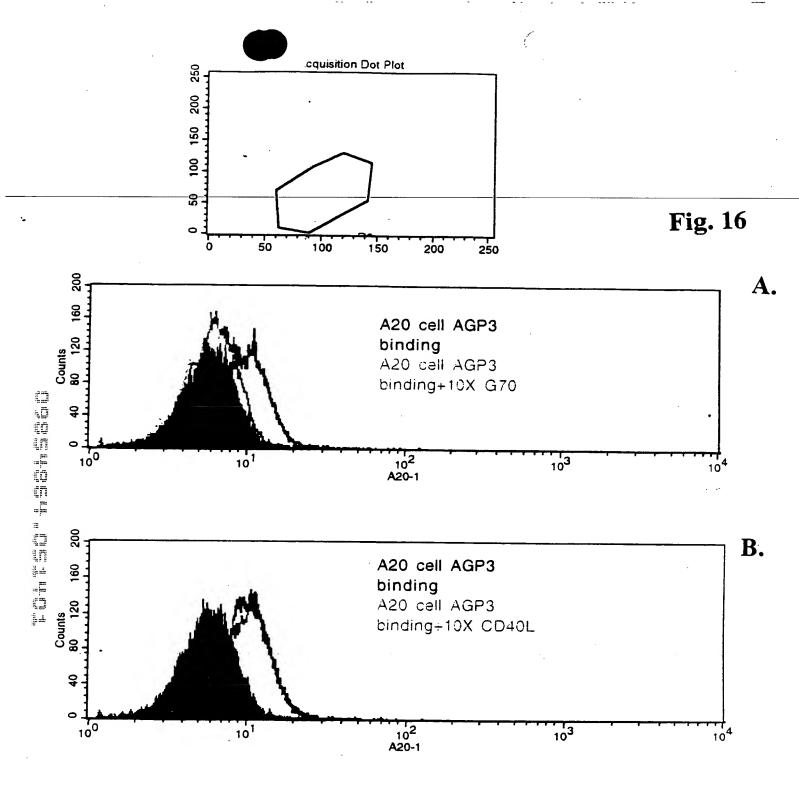
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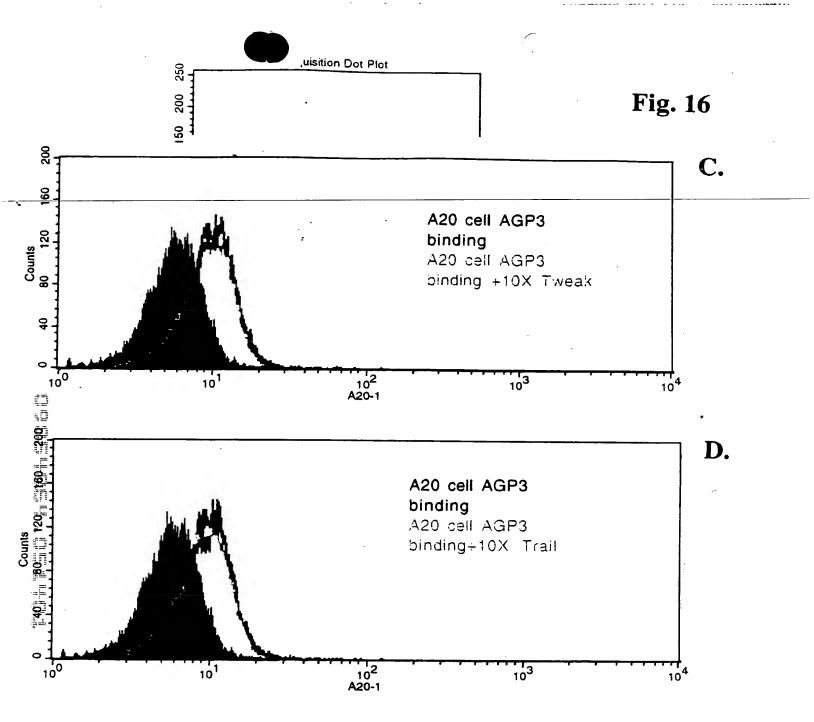
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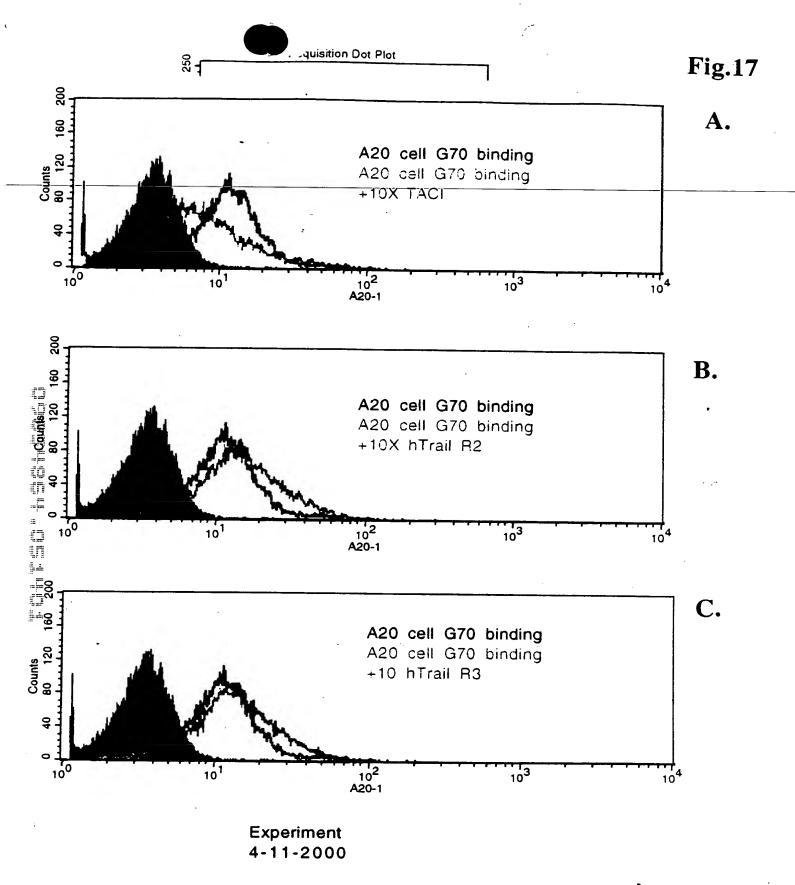
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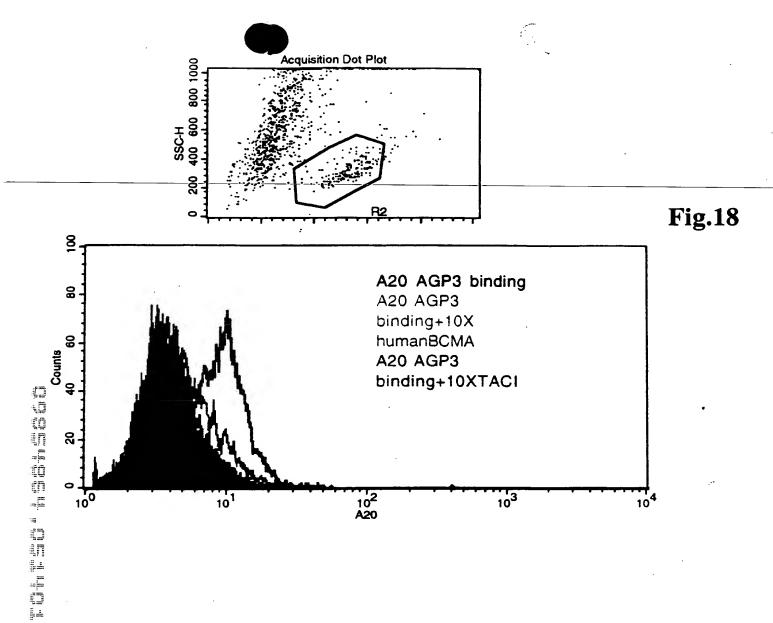


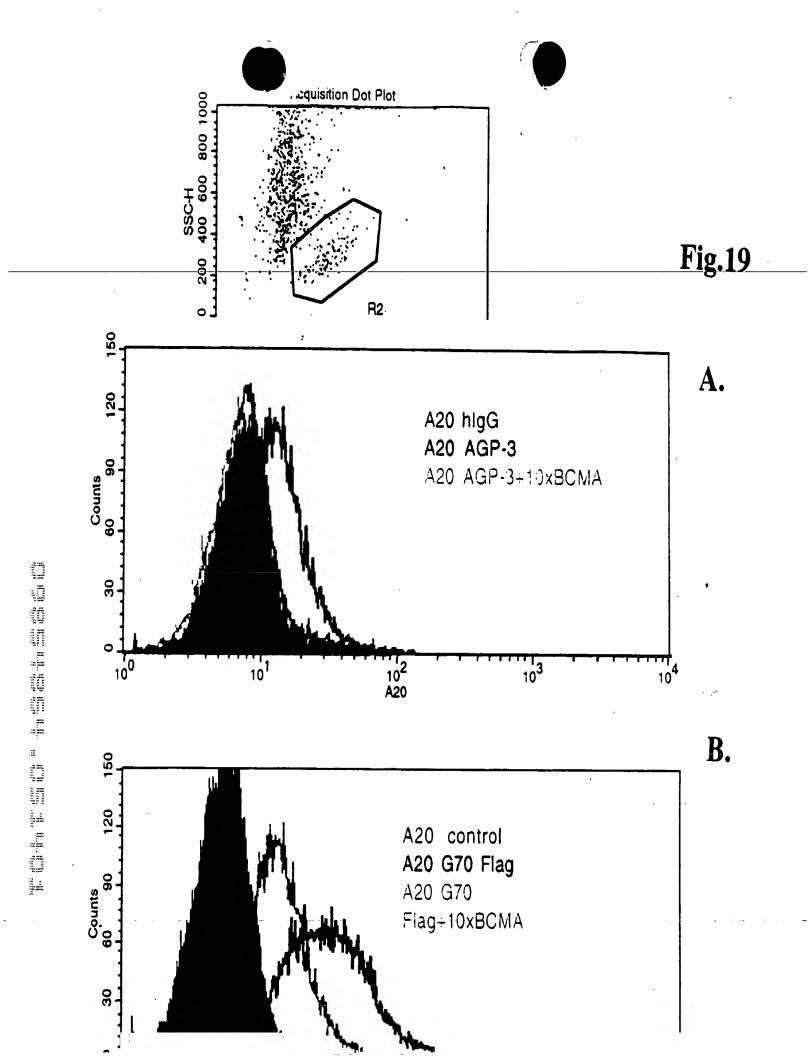
Experiment 4-3-2000



Experiment 4-3-2000







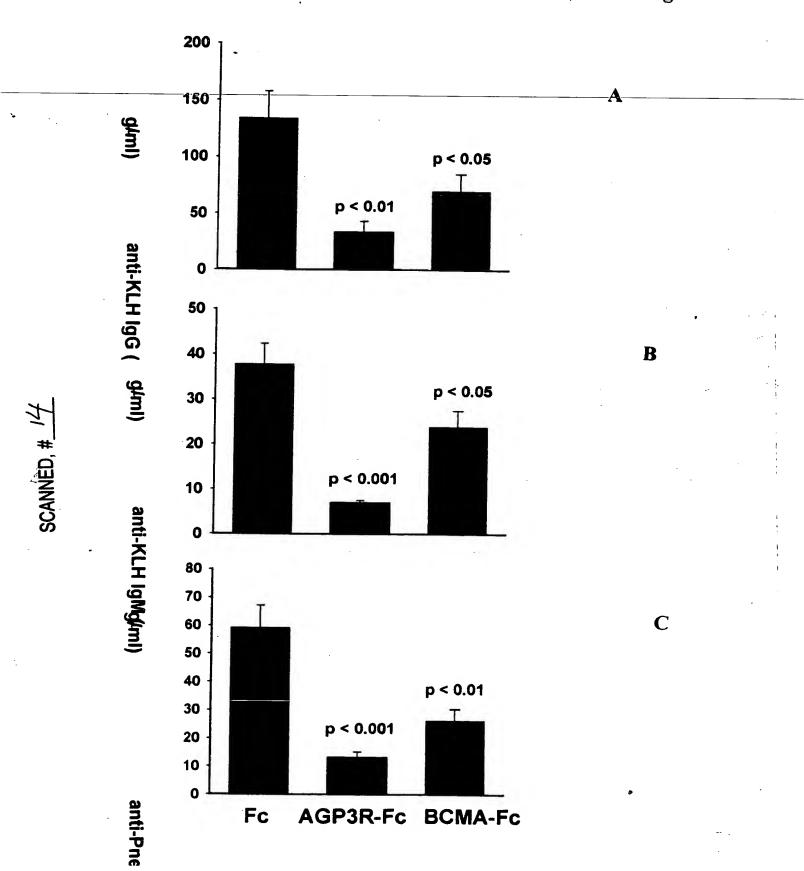


Figure 21 Fc-humanAPRIL

ol site)

Fc-human and April:	nAPRIL protein sequ	ience including the	signal sequence, Fc	Fc-humanAPRIL protein sequence including the signal sequence, Fc domain, linker (Xhol sitr and April:
Т	MEWSWVFLFF	LSVTTGVHSD	KTHTCPPCPA	PELLGGPSVF
	LFPPKPKDTL			
51	MISRTPEVTC	VVVDVSHEDP	EVKFNWYVDG	VEVHNAKTKP
	REEQYNSTYR			
101	VVSVLTVLHQ	DWLNGKEYKC	KVSNKALPAP	IEKTISKAKG
	QPREPQVYTL			
151	PPSRDELTKN	QVSLTCLVKG	FYPSDIAVEW	ESNGQPENNY
	KTTPPVLDSD			
201	GSFFLYSKLT	VDKSRWQQGN	VFSCSVMHEA	LHNHYTQKSL
	SLSPGKSRAV			
251	LTQKQKKQHS	VLHLVPINAT	SKDDSDVTEV	MWQPALRRGR
	GLQAQGYGVR			
301	IQDAGVYLLY	SQVLFQDVTF	TMGQVVSREG	QGRQETLFRC
	IRSMPSHPDR			
351	AYNSCYSAGV	FHLHQGDILS	VIIPRARAKL	NLSPHGTFLG
	FVKL*			

Figure 22

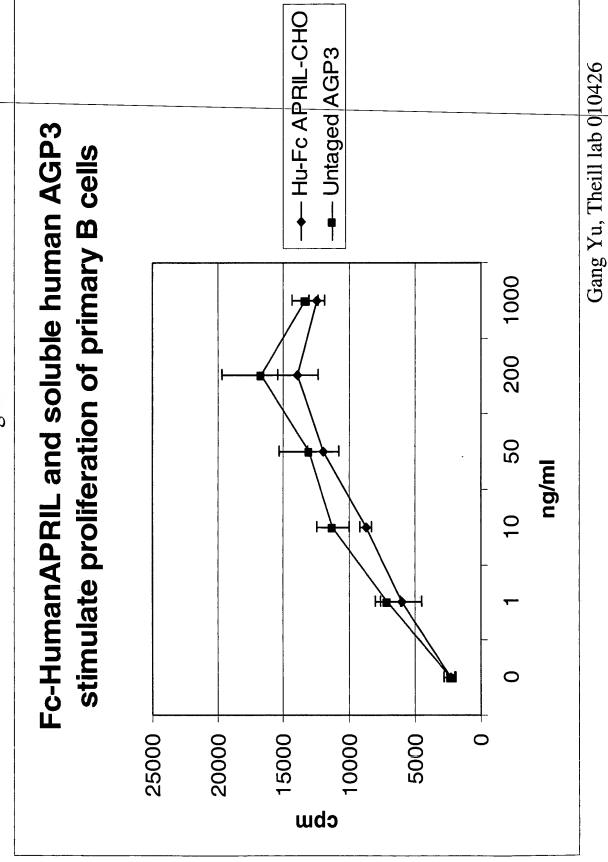


Figure 23

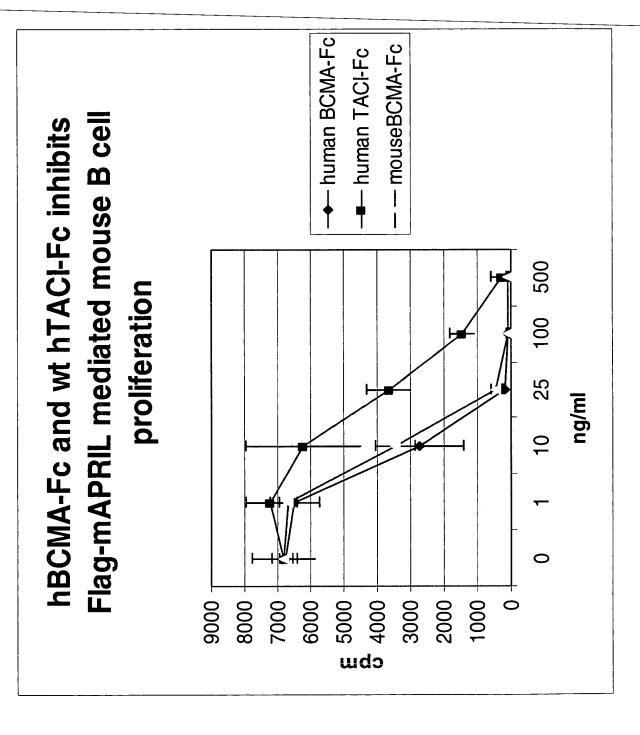


Figure 24:

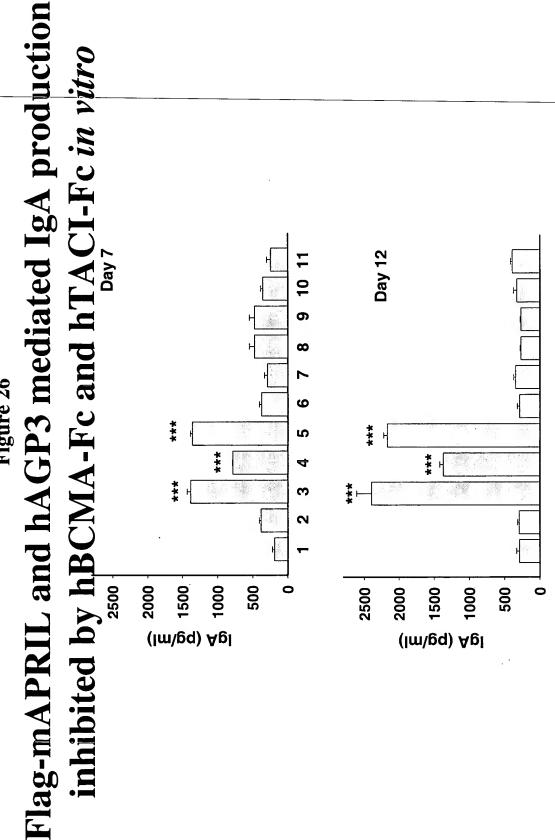
hBCMA-Fc reduces PB	educe	educes PB B cell	3, and 6	B cell level in vivo
BLOOD	WBC 10e6/ml	# Lym 10e6/ml	CD3+	CD3-B220+
BCMA-Fc	5.30	3.81	2.3	1.3
SD	0.39	0.43	0.32	0.27
t test	0.03318	0.01570	0.24737	0.00506
L	00	6.43	7.6	3.0
OS -	1.27	1.52	9.0	
Saline	06.9	5.55	2.1	2.9
SD	2.04	1.79	0.5	1.2
			THE STATE OF THE S	

Figure 25

hBCMA-Fc reduces spleen B cell levels in vivo

spleen	WBC	Lym	spleen lym# CD3-B220+	CD3-B220+	CD3-B220+
1	10e6/ml	(%)	10ml(x10e6)	(%)	#
BCMA-Fc	9.12	97.9	89.3	45.5	41.8
SD	0.92	0.51	9.32	1.29	4.92
t test	0.02778	0.89118	0.02668	0.00234	0.02088
FC	11.49	97.9	112.5	50.6	57.1
SD	1.62	0.38	15.65	1.95	9.67
Saline	11.48	98.5	113.1	53.7	48.5
OS	1.71	0.1	16.9	6.7	29.15

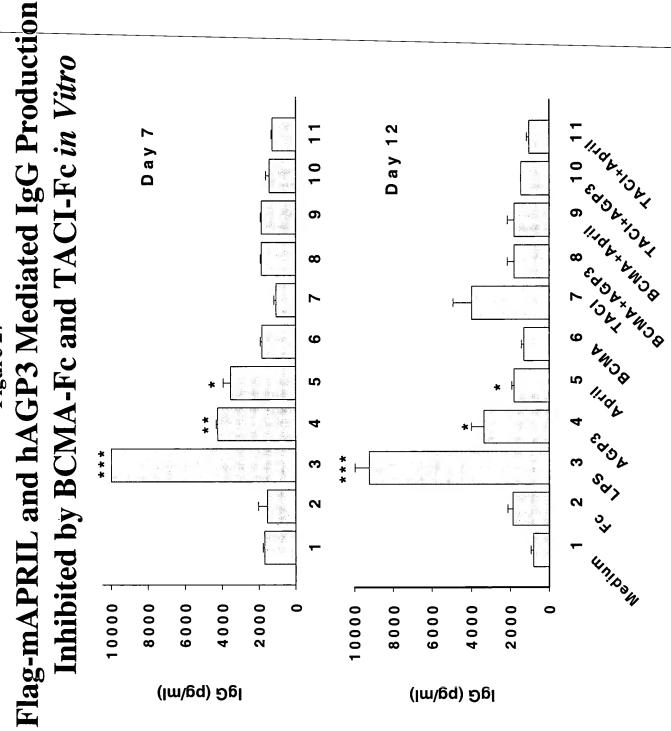
Figure 26



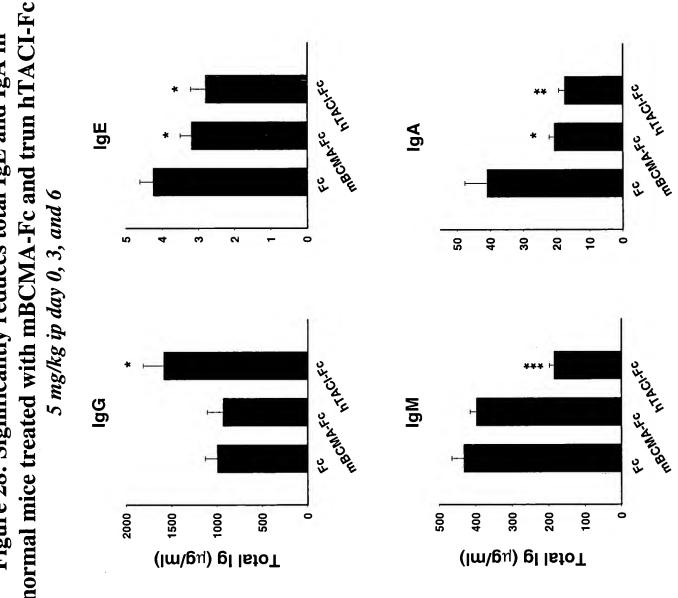
Mdy John

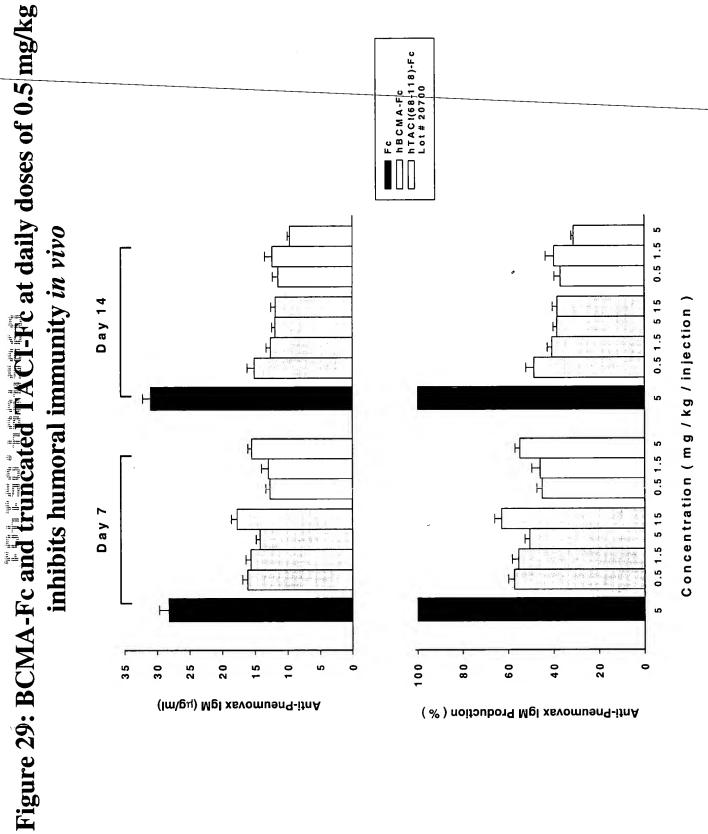
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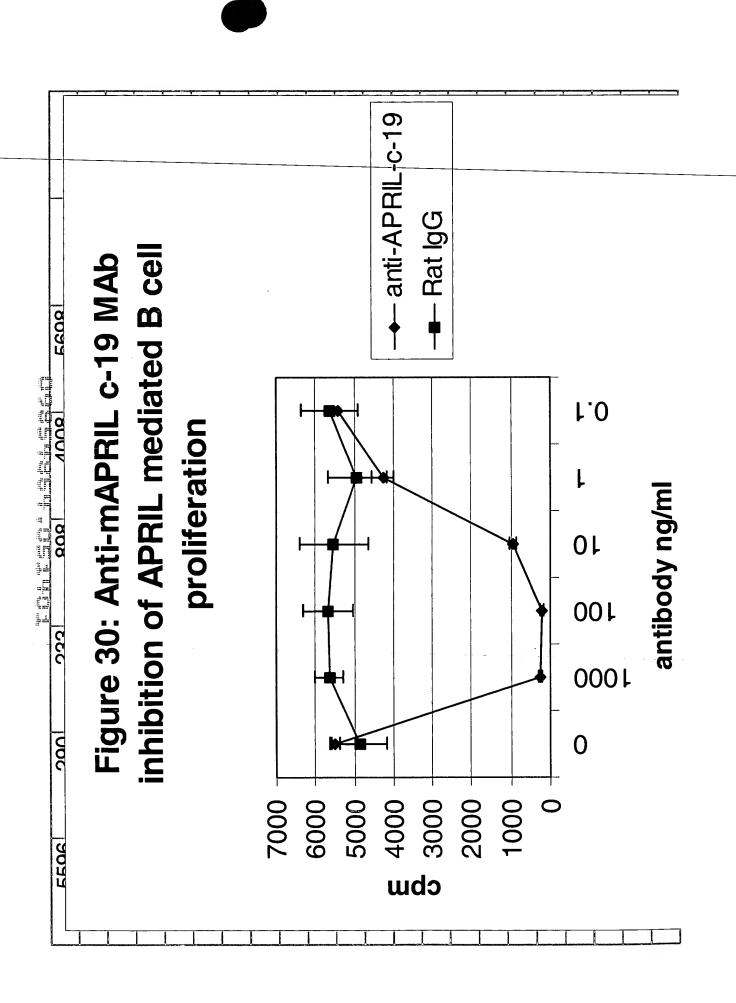
Figure 27



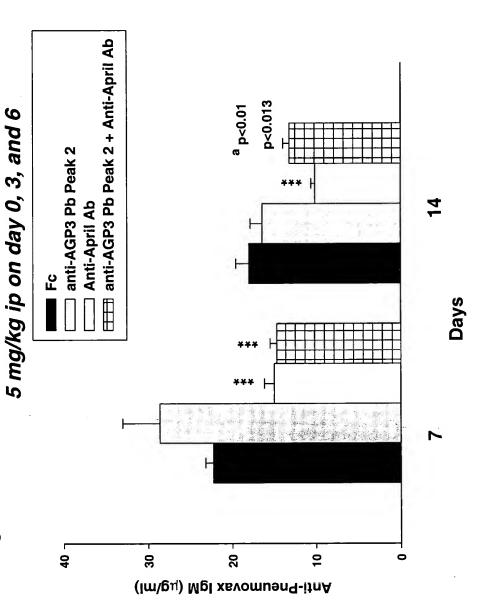
normal mice treated with mBCMA-Fc and trun hTACI-Fc Figure 28: Significantly reduces total IgE and IgA in



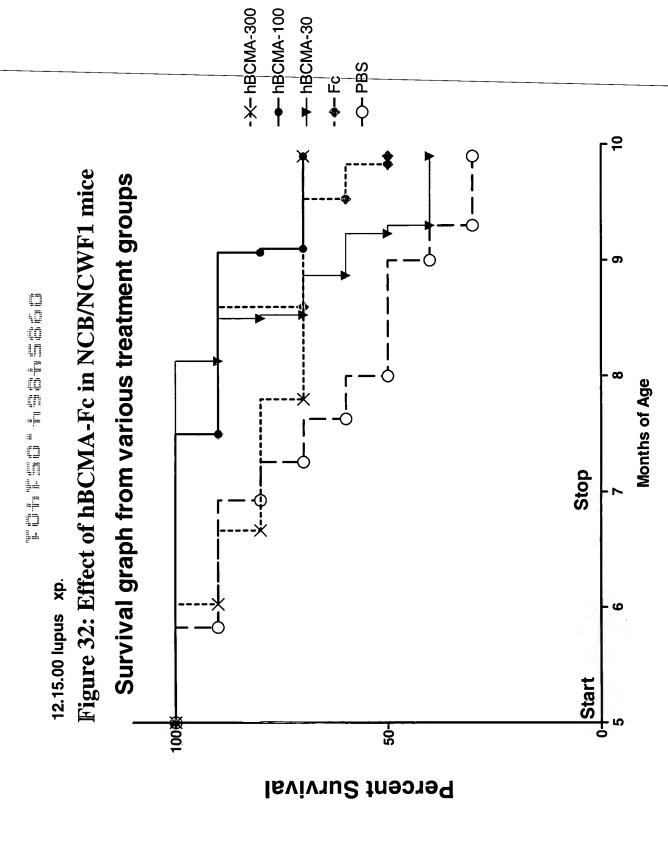




Neutralizing anti-mAPRIL Mab Reduces anti-Pheumovacs IgM In Vivo Figure 31



^a difference between Anti-April Ab and anti-AGP3 Pb Peak 2+ Anti-April Ab Groups

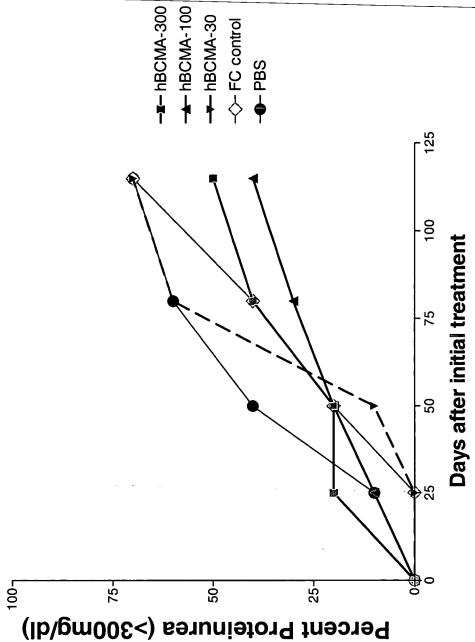


N=10 Mice were treated for 8 weeks 3x/week with the indicated proteins. KIN2 group had 12 mice. The 100 in the legend stands for 100 µg of protein or 4mg/kg i.p.

12.15.00 lupus xp

Figure 33: Effect of hBCMA-Fc in NCB/NCWF1 mice

Percentage of mice with proteinurea (>300mg/dl) from various treatment groups



N=10 Five month old BWF1 mice were treated with protein for 8 weeks i.p. The hBCMA-300 stands for hBCMA-fc 300µg/mouse (12mg/kg)

Figure 34: Analysis of antibodies to dsDNA from the peripheral blood from various treatment groups of BWF1 at day 0,30,60, and 90.

	MEAN	anti-de	SDNA is	sotype	MEAN anti-dsDNA isotypes in U/ml	٦		
Andrea de la companya de la company	Day 0		Day 30		Day 60		Day 90	
Group #	IgG	IgM	lgG	IgM	lgG	IgM	lgG	IgM
hBCMA-300	179	260	163	371	150	902	171	841
hBCMA-100	150	430	259	718	171	822	339	1031
hBCMA-30	377	265	297	458	401	664	424	601
G	149	371	234	283	384	331	432	351
PBS	308	292	439	311	247	276	720	467
	Standa	ard De	viation	of the	Standard Deviation of the above means	means		
	Day 0		Day 30		Day 60		Day 90	
Group #) Jg	MgI	lgG	Ngi	lgG	IgM	lgG	Mg
hBCMA-300	104	303	116	211	62	518	62	734
hBCMA-100	109	292	306	461	212	758	371	1225
hBCMA-30	363	455	281	430	305	909	421	400
J.	89	160	150	င္တ	391	151	233	237
PBS	311	73	474	152	247	370	870	327

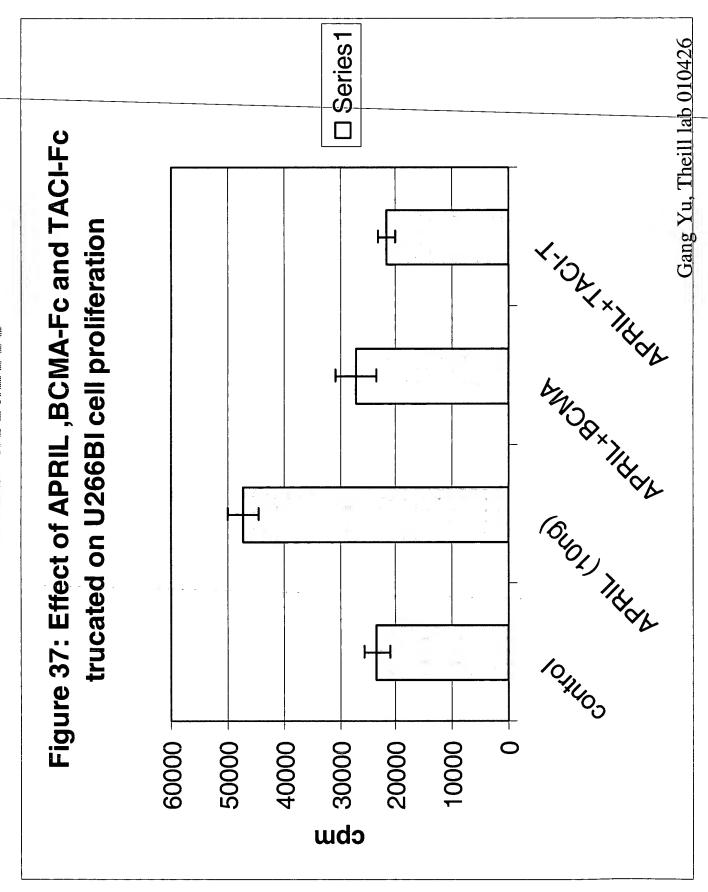
the12mg/kg (30 ug), 4mg/kg (100ug), and 1.3mg/kg (300 ug) dose of Figure 35: Evaluation of B cell numbers at treatment day 60 from hBCMA-Fc groups along with the Fc and PBS control groups.

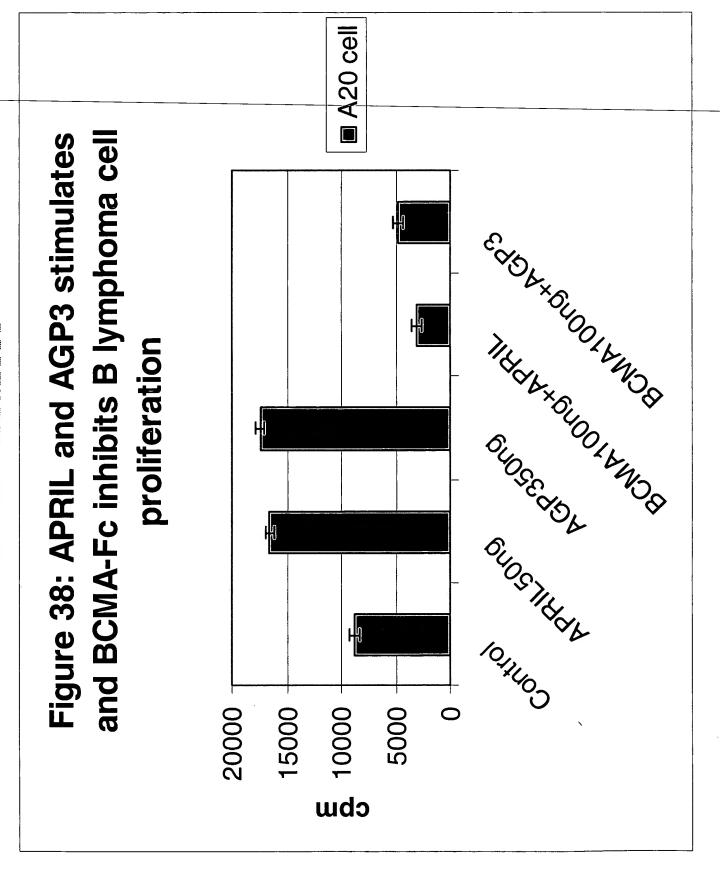
hBCMA-fc-300	>-300			hBCMA-100	00			hBCMA-FC-30	C-30		
Mouse#	%CD4	%CD8	%B220		%CD4	%CD8	%B220		%CD4	%CD8	%B220
1.0	16.3	11.0	16.4	5.0	26.1	14.9	10.1	9.0	2.5	6.9	10.3
2.0	24.1	11.1	11.6	0.9	21.1	11.3	10.6	10.0	13.2	ģ.2	23.4
3.0	18.2	7.4	9.6	7.0	24.6	13.3	8.3	11.0	15.9	6.4	29.2
4.0	25.4	13.3	13.1	8.0	20.0	11.3	13.4	12.0	14.8	9.7	31.5
×	21.0	10.7	12.8	×	23.0	12.7	10.6	×	11.6	6.5	23.6
8	4.4	2.4	2.8	छ	2.9	1.7	2.1	क्र	6.2	1.0	9.5
Fc				PBS							
33.0	7.0	8.1	25.4	37.0	16.9	8.3	15.5				
34.0	10.7	4.9	15.3	38.0	19.1	12.1	19.5				
35.0	18.9	9.3	21.0	39.0	7.1	3.4	17.5				
36.0	20.1	11.1	21.0	40.0	19.9	11.4	26.5				
×	14.2	8.4	20.7	×	15.8	8.8	19.8				
ଞ	6.4	2.6	4.1	bs	5.9	4.0	4.8				

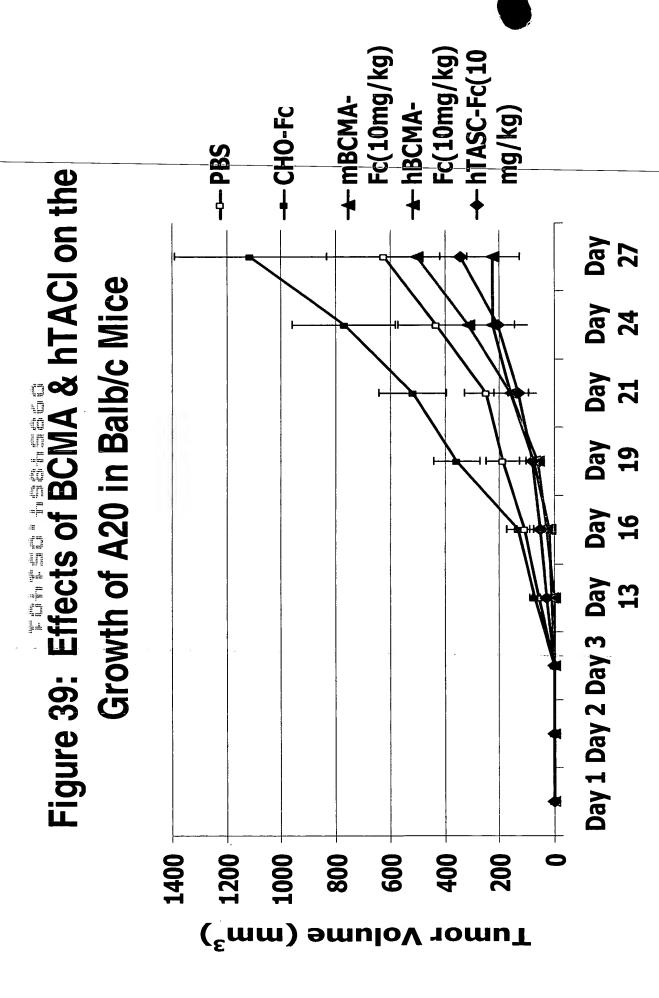
Figure 36: Specific APRIL binding to Human Cell lines determined by FACS analysis

APRIL binding

noma + +	- + +	cinoma ++	++	++	oma ++	+ +	noma	1	arcinoma
HT 29 Colon adenocarcinoma	NCI 460 Lung carcinoma	PC3 Prostate adennocarcinoma	C6 Glial carcinoma	Raji Burkitt lymphoma	A20 Mouse B cell lymphoma	U266BI Myeloma	A435 Epidermoid carcinoma	A469 Kidney carcinoma	MDA-231 breast adenocarcinoma

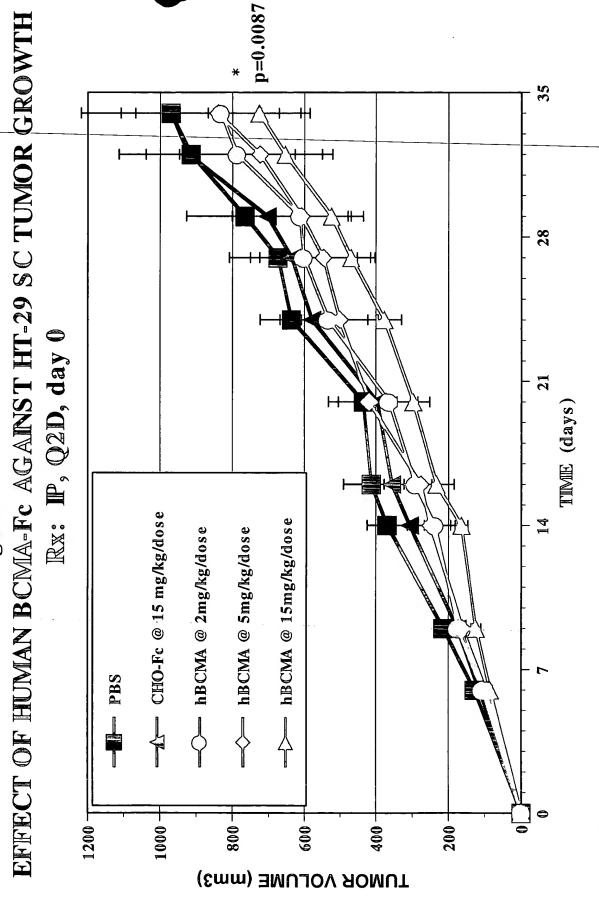






Days After Tumor Implantation

EFFECT OF HUMAN BCMA-FC AGAINST HT-29 SC TUMOR GROWTH ronran hasnaser Figure 40



Linear growth ANOVA with Dunnett's correction for multiple testing (n=10/group)

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